

OIPE

RAW SEQUENCE LISTING

DATE: 10/18/2001

PATENT APPLICATION: US/09/965,313

TIME: 16:18:36

Input Set : A:\Sequencing Listing as filed.txt

Output Set: N:\CRF3\10182001\I965313.raw

ENTERED

2.

4 <110> APPLICANT: Hodge, Martin R.
6 <120> TITLE OF INVENTION: Novel IL-9/IL-2 Receptor-Like Molecules
7 and Uses Thereof
9 <130> FILE REFERENCE: 5800-17A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/965,313
C--> 11 <141> CURRENT FILING DATE: 2001-09-26
11 <150> PRIOR APPLICATION NUMBER: US 09/313,913
12 <151> PRIOR FILING DATE: 1999-05-18
14 <160> NUMBER OF SEQ ID NOS: 8
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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19 <211> LENGTH: 2343
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (349)...(1962)
27 <400> SEQUENCE: 1
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29 cgcctggtag ctcccttgcc gtctctttcc tctgtctgct gctctgtggg acacctgcct 120
30 ggaggcccag ctgcccgta tcagagtgc aggtcttatg acagcctgat tggtagctcg 180
31 ggctgggtgt ggattctcac ccagggcctc tgcctgcttt ctacagacct catctgtcac 240
32 cccacgctg aacccagctg ccaccccgag aagcccatca gactgcccc agcacacgga 300
33 atggatttct gagaaagaag ccgaaacaga aggcccgtgg gagtcagc atg ccg cgt 357
34 Met Pro Arg
35 1
37 ggc tgg gcc gcc ccc ctg ctc ctg ctg ctg ctc cag gga ggc tgg ggc 405
38 Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly Gly Trp Gly
39 5 10 15
41 tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg gtc atc tgc 453
42 Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys
43 20 25 30 35
45 atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc ctt acc tgg 501
46 Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp
47 40 45 50
49 caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc 549
50 Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu
51 55 60 65
53 cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg 597
54 His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
55 70 75 80
57 gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca 645
58 Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
59 85 90 95
61 gac cag tct ggc aac tac tcc cag gag tgt ggc ttt ctc ctg gct 693
62 Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala
63 100 105 110 115

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65	gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg acc ttc tca	741
66	Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser	
67	120 125 130	
69	gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc	789
70	Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe	
71	135 140 145	
73	tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac cgg	837
74	Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg	
75	150 155 160	
77	gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg gac	885
78	Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp	
79	165 170 175	
81	tca aga agt gtc tcc ctc ccc ctg gag ttc cgc aaa gac tcg agc	933
82	Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser	
83	180 185 190 195	
85	tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag	981
86	Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln	
87	200 205 210	
89	ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca	1029
90	Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser	
91	215 220 225	
93	gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt ctc ctc ctg	1077
94	Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu Leu	
95	230 235 240	
97	ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag acc cat cca	1125
98	Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His Pro	
99	245 250 255	
101	ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc cct gag cgg	1173
102	Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu Arg	
103	260 265 270 275	
105	ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc aag aaa tgg	1221
106	Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys Trp	
107	280 285 290	
109	gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga ccc tgg agc	1269
110	Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp Ser	
111	295 300 305	
113	cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac cca cga cgg	1317
114	Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro Arg	
115	310 315 320	
117	agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa cca gca gag	1365
118	Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala Glu	
119	325 330 335	
121	ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg ccg aca gcc	1413
122	Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr Ala	
123	340 345 350 355	
125	cag aac tcg ggg ggc tca gct tac agt gag gag agg gat cgg cca tac	1461
126	Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro Tyr	
127	360 365 370	
129	ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca gag ggg cca	1509

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130 Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly Pro
131          375          380          385
133 tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca gcc ctg gac      1557
134 Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu Asp
135          390          395          400
137 ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac cca ctc ttg      1605
138 Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu Leu
139          405          410          415
141 gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca gct ggc agc      1653
142 Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly Ser
143          420          425          430          435
145 cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag cca      1701
146 Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys Pro
147          440          445          450
149 ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt ggc      1749
150 Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly Gly
151          455          460          465
153 cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg gcc      1797
154 Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu Ala
155          470          475          480
157 ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac tgc      1845
158 Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp Cys
159          485          490          495
161 agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga ccc      1893
162 Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly Pro
163          500          505          510          515
165 ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt tcg      1941
166 Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu Ser
167          520          525          530
169 agc cct gga ccc cag gcc agc taatgaggct gactggatgt ccagagctgg      1992
170 Ser Pro Gly Pro Gln Ala Ser
171          535
173 ccaggccact gggccctgag ccagagacaa ggtcacctgg gctgtgatgt gaagacacct      2052
174 gcagcctttg gtctcctgga tgggcctttg agcctgatgt ttacagtgtc tgtgtgtgtg      2112
175 tgtgcatatg tgtgtgtgtg catatgcatg tgtgtgtgtg tgtgtgtctt aggtgocgag      2172
176 tggcatgtcc acgtgtgtgt gtgattgcac gtgcctgtgg gcctgggata atgcccattg      2232
177 tactccatgc attcacctgc cctgtgcatg tctggactca cggagctcac ccattgtgcac      2292
178 aagtgtgcac agtaaactgt tttgtggtca aaaaaaaaaa aaaaaaaaaa a      2343
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 538
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like
185 <400> SEQUENCE: 2
186 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly
187 1          5          10          15
188 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
189          20          25          30
190 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
191          35          40          45

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192 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
193      50                      55                      60
194 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
195 65                      70                      75                      80
196 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
197                      85                      90                      95
198 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
199                      100                      105                      110
200 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
201                      115                      120                      125
202 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
203 130                      135                      140
204 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
205 145                      150                      155                      160
206 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
207                      165                      170                      175
208 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
209                      180                      185                      190
210 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
211                      195                      200                      205
212 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
213 210                      215                      220
214 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
215 225                      230                      235                      240
216 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
217                      245                      250                      255
218 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
219                      260                      265                      270
220 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
221                      275                      280                      285
222 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
223                      290                      295                      300
224 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
225 305                      310                      315                      320
226 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
227                      325                      330                      335
228 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
229                      340                      345                      350
230 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
231                      355                      360                      365
232 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
233 370                      375                      380
234 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
235 385                      390                      395                      400
236 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
237                      405                      410                      415
238 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
239                      420                      425                      430
240 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg

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```

241          435          440          445
242 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
243          450          455          460
244 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
245          465          470          475          480
246 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
247          485          490          495
248 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
249          500          505          510
250 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
251          515          520          525
252 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
253          530          535
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 2456
257 <212> TYPE: DNA
258 <213> ORGANISM: Mus musculus
260 <220> FEATURE:
261 <221> NAME/KEY: CDS
262 <222> LOCATION: (391)...(1977)
264 <400> SEQUENCE: 3
265 cagctgtctg cccaattctc ctgtggtgtg cctcacggtc acttgcttgt ctgaccgcaa      60
266 gtctgcccac ccttggggca gccaaactggc ctcagcccggt gccccaggcg tgccctgtct      120
267 ctgtctggct gccccagccc tactgtcttc ctctgtgtag gctctgcccga gatgcccggc      180
268 tggtcctcag cctcaggact atctcagcag tgactcccct gattctggac ttgcacctga      240
269 ctgaactcct gccacactca aaccttcacc tcccaccacc accactccga gtcccgtgt      300
270 gactcccacg cccaggagac cacccaagtg cccagccta aagaatggct ttctgaggaa      360
271 gatcctgaag gagtaggtct gggacacagc atg ccc cgg ggc cca gtg gct gcc      414
272                                     Met Pro Arg Gly Pro Val Ala Ala
273                                     1           5
275 tta ctc ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act      462
276 Leu Leu Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr
277      10           15           20
279 tgc tac act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg      510
280 Cys Tyr Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg
281      25           30           35           40
283 agc ccc aac ccc agc ata ctc agt ctc acc tgg caa gat gaa tat gag      558
284 Ser Pro Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu
285          45           50           55
287 gaa ctt cag gac caa gag acc ttc tgc agc cta cac aag tct ggc cac      606
288 Glu Leu Gln Asp Gln Glu Thr Phe Cys Ser Leu His Lys Ser Gly His
289          60           65           70
291 aac acc aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc      654
292 Asn Thr Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe
293          75           80           85
295 ctg tcc gat gaa gtt ttc att gtc aac gtg acg gac cag tct ggc aac      702
296 Leu Ser Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn
297          90           95          100
299 aac tcc caa gag tgt ggc agc ttt gtc ctg gct gag agc atc aag cca      750

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date